

1 CCCACGGCTC CGCATAAATC AGCAGCGGCG CGGAGAACC CGCTCTTGGG GCGTTAGAGA CGCGGTGTTT TTATGTGGCT GCTACGGGCT AGATGAAATT CCCGACTTTG
GGGTGGCAG GCGTATTTAG TCGTGGCGCG GCCTCTTGGG GCGTTAGAGA CGCGGTGTTT TTATGTGGCT GCTACGGGCT AGATGAAATT CCCGACTTTG
101 CCACGGGCTT GAGAGACTAT AAGAGCGTTC CCTACCGCCA TGGAAACAAC GGGACAGAAC GCGCGGCGCG CTTTCGGGGG CCGGAAAAGG CACGGCCCCAG
GGTGGCCCGA CTCTCTGATA TTCTCGCAAG GGATGGCGGT ACCTTGTTCG CCGTGTCTTG CGGGCGCGG GAAAGCCCGG GGCCTTTTCC GTGCCGGGTC
201 GACCCAGGGA GCGCGGGGA GCCAGGCGCTG GCGTCCGGGT CCCAAGACC CTTGTGCTCG TTGTGCGCGG GTTCCTGCTG TTGGTCTCAG CTGAGTCTGC
CTGGGTCCCT CCGCGCCCT CCGTCCGGAC CCGAGGCCCA GGGGTTCTGG GAAACAGAGC AACAGCGCGG CCAGGACGAC AACACAGATC GACTCAGACG
22 ProArgG1 uAlaArgGly AlaArgProG lYLeuArgVa lProLysThr LeuValLeuV alValAlaAl aValLeuLeu LeuValSerA laGluSerAla
301 TCTGATCACC CAACAAGACC TAGTCCCCA GCAGAGAGCG GCGCCACAAC AAAAGAGGTC CAGCCCTCA GAGGGATTGT GTCCACCTGG ACACCATATC
AGACTAGTGG GTTGTCTGG ATCGAGGGGT CGTCTCTCGC CCGGGTGTG TTTTCTCCAG GTCGGGAGT CTCCCTAACA CAGGTGGACC TGTGGTATAG
55 LeuIleThr GlnGlnAspL euAlaProG l nGlnArgAla AlaProGlnG l nLysArgSe rSerProSer GluGlyLeuC ysProProG l yHisHisIle
401 TCAGAAGACG GTAGAGATTG CATCTCTGTC AAATATGGAC AGGACTATAG CACTCACTGG AATGACCTCC TTTTCTGCTT CCGCTGCACC AGGTGTGATT
AGTCTTCTGC CATCTCTAAC GTAGAGGACG TTTATACCTG TCCTGATATC GTGAGTGACC TTACTGGAGG AAAAGACGAA CCGACGTGG TCCACACTAA
88 SerGluAspG lYArgAspCy sIleSerCys LysTyrGlyG l nAspTyrSe rThrHisTrp AsnAspLeuL euPheCysLe uArgCysThr ArgCysAspSer
501 CAGGTGAAGT GGAGCTAAGT CCCTGCACCA CGACCAGAAA CACAGTGTGT CAGTGGGAGG AAGGCACCTT CCGGGAAGAA GATTCTCTCTG AGATGTGCCG
GTCCACTTCA CCTCGATTCA GGGACGTGGT GCTGGTCTTT GTGTACACA GTACCGCTTC TTCCGTGGAA GGCCCTTCTT CTAAGAGGAC TCTACACGGC
122 GlyGluVa lGluLeuSer ProCysThrT hrThrArgAs nThrValCys GlnCysGluG luGlyThrPh eArgGluGlu AspSerProG luMetCysArg
601 GAAGTGGCG ACAGGGTGT CCAGAGGGAT GGTCAAGGTC GGTGATTGTA CACCTCGAG TGACATCGAA TGTGTCCACA AAGAATCAGG CATCATCATA
CTTCACGGCG TGTCCACAG GGTCTCCCTA CAGTTCCAG CCCTAACAT GTGGGACCTC ACTGTAGCTT ACACAGGTGT TTTCTTAGTCC GTAGTAGTAT
155 LysCysArg ThrGlyCysP roArgGlyMe tValLysVal GlyAspCysT hrProTrpSe rAspIleGlu CysValHisL ysGluSerG l yIleIleIle
701 GGAGTCACAG TTGCAGCCGT AGTCTTGATT GTGGTGTGT TTGTTTGCAA GTCTTTACTG TGAAGAAAG TCCTTCTCTTA CCTGAAAGGC ATCTGCTCAG
CCTCAGTGT CACGTGGCA TCAGAACTAA CACGACACA CACCAACGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCCG TAGACGAGTC
188 GlyValThrV alAlaAlaVa lValLeuIle ValAlaValP heValCysLy sSerLeuLeu TrpLysLysV alLeuProTy rLeuLysGly IleCysSerGly
801 GTGTGGTGG GGACCTGAG CGTGTGGACA GAAGCTACA ACGACCTGG GCTGAGGACA ATGTCTCTCAA TGAGATCGTG AGTATCTTGC AGCCACCCCA
CACCACACC CCTGGGACT GCACACCTGT CTTCGAGTGT TGCTGGACCC CGACTCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACC TCGGGTGGGT
222 GlyGlyG lYAspProGlu ArgValAspA rgSerSerG l nArgProGly AlaGluAspA snValLeuAs nGluIleVal SerIleLeuG lnProThrGln

FIG. 1A

901 GGTCCTCTGAG CAGGAAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCCGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA
 CCAGGGACTC GTCCCTTTACC TTCAGGTCCT CGGTCTCTC GGTGTCCAC AGTTGTACAA CAGGGGGCCC CTCAGTCTCG TAGACGACCT TGGCCGTCTT
 255 ValProGlu GlnGluMetG luValGlnG1 uProAlaGlu ProThrGlyV alAsnMetLe userProGly GluSerGluH isLeuLeuG1 uProAlaGlu
 1001 GCTGAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TCCCACTGAG ACTCTGAGAC AGTGTTCGA TGACTTTGCA GACTTGGTGC
 CGACTTTCCA GAGTCTCCTC CTCGACGAC CAAGTCTGTT TACTTCCACT AGGTGACTC TGAGACTCTG TCACGAAGCT ACTGAAACGT CTGAACCACG
 288 AlaGluArgS erGlnArgAr gArgLeuLeu ValProAlaA snGluGlyAs pProThrGlu ThrLeuArgG lnCysPheAs pAspPheAla AspLeuValPro
 1101 CCTTTGACTC CTGGGAGCCG CTCATGAGGA AGTTGGGCT CATGGACAAT GAGATAAAGG TGGCTAAAGC TGAGGCAGCG GGCCACAGGG ACACCTTGTA
 GGAAACTGAG GACCCTCGGC GAGTACTCCT TCACACCCGGA GTACCTGTTA CTCATTTC ACCGATTTCG ACTCCGTCCG CCGGTGTCCC TGTGGAACAT
 322 PheaspSe rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluIleLysV alAlaLysAl aGluAlaAla GlyHisArgA spThrLeuTyr
 1201 CACGATGCTG ATAAAGTGGG TCAACAAAAC CGGGCGAGAT GCCTCTGTCC ACACCCCTGTG GAGACGCTGG GAGAGAGACT TGCCAAGCAG
 GTGCTACGAC TATTTCACCC AGTTGTTTTG GCCCGCTCTA CGGAGACAGG TGTGGGACGA CCTACGGAAC CTCTGCGACC CTCTCTCTGA ACGGTTCGTC
 355 ThrMetLeu IleLysTrpV alAsnLysTh rGlyArgAsp AlaSerValH isThrLeuLe uAspAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln
 1301 AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGTTCATGT ATCTAGAAGG TAATGCAGAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA
 TTCTAACTCC TGGTGAACAA CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGTCTG AGACGGAACA GGATTCACAC TAAGAGAAAGT CCTTCACCTCT
 388 LysIleGluA spHisLeuLe uSerSerGly LysPheMetT yrLeuGluG1 yAsnAlaAsp SerAlaXaaS erOC*
 1401 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CCGTACTGGA AGAAACTCTC
 GGAAGGGACC AAATGGAAAA AAGACCTTTT TCGGGTTGAC CTGAGGTCAG TCATCCTTTC ACGGTGTTAA CAGTGTACTG GCCATGACCT TCTTTGAGAG
 1501 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACCT TTCACTGCCAC TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAT
 GGTAGGTTGT AGTGGGTCAC CTACCTTGTA GGACATTGAA AAGTGACGTG AACCGTAATA AAAATATTTCG ACTTACACTA TTATTCTCTGT GATACCTTTA
 1601 GTCTGGATCA TTCCGTTTTGT GCGTACTTTG AGATTGGTT TGGGATGTC TTTTITTCAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT
 CAGACCTAGT AAGGCAACA CGCATGAAAC TCTAAACCAA ACCCTACAGT AACAAAAGTG TCGTGAAAAA ATAGATTAC ATTACGAAA TAAATAAATA
 1701 TTGGGTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA GCGGCGCGG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC
 AACCCGATGT AACATTCTAG GTAGATGTTT TTTTTTTTTT TTTTTTTTTT CCGCCGGCGC TGAGATCTCA GCTGGACGTC TTCGAAACCGG CGGTACCGG

FIG. 1B

1 MEQRGONAPAAAGARKRHGPGPREARGARGLRVPKTLVLVVAALLLVSAESALITQQD
61 LAPQORAAPOQKRSSPSEGLCPPGHHISEDGRDCISCKYQDYSTHWNDLLFC_LRCRTRCD
121 SGEVELSPCTTTRNTVCQCEEGTFREEDSPENCRKCRGTGCPRGWVKVGDCTPWSDIECVH
181 KESGIIIGVTVAAVLIVAVFVCKSLMVKVLPYLKGCISGGGGDPERVDRSSQRPGEAD
241 NVLNEIVSILQPTQVPEQEMEVEQPEAPTGVNMLSPGESEHLLLEPAEAERSQRRRLVPA
301 NEGDPTE_TL_RQC_FDDFADLV_PFD_SWEPLMRKLG_LMDNEIKVAKAEAGHRDTLT_YTMLIKW
361 VNKTGRDASVHTLLDALETLGERLAKQKIEDHLLSSGKFMYLEGNADSALS

FIG._2A

Apo2	FADLV	VPFDS	WEP	LMR	KKLG	LM	DNEIK	VAKAE	AA--	GHRDTL
DR4	FANIV	PFDS	WDL	MRQL	DLTK	NEID	VVRAG	TA--	GGDA	L
Apo3/DR3	VMDA	VPA	RRWK	EFVR	TGL	REAE	EAEVE	IGR--	FRDQ	Q
TNFR1	VVEN	VPP	PLRW	KEFV	RLGL	SDHE	IDRL	ELQNG	R--	CLREA
Fas/Apo1	IAGV	MTLS	QVK	GFVR	KNG	VNEAK	ID	EIKND	NVQD	TAEQKV

Apo2	YTM	LIK	WV	NK	TGR	D--	ASV	HTLL	DALE	ETL	GERL	AKQK	IED
DR4	YAM	LM	KW	VN	K	TGR	N--	AS	IHT	LLDA	LER	MEER	HAK
Apo3/DR3	YEM	L	K	R	W	R	Q	Q	P--	--	AGL	GAV	YA
TNFR1	YSM	L	A	T	W	R	R	R	T	P	R	REA	T
Fas/Apo1	-Q	L	L	R	N	W	H	Q	L	H	G	K	E

FIG._2B

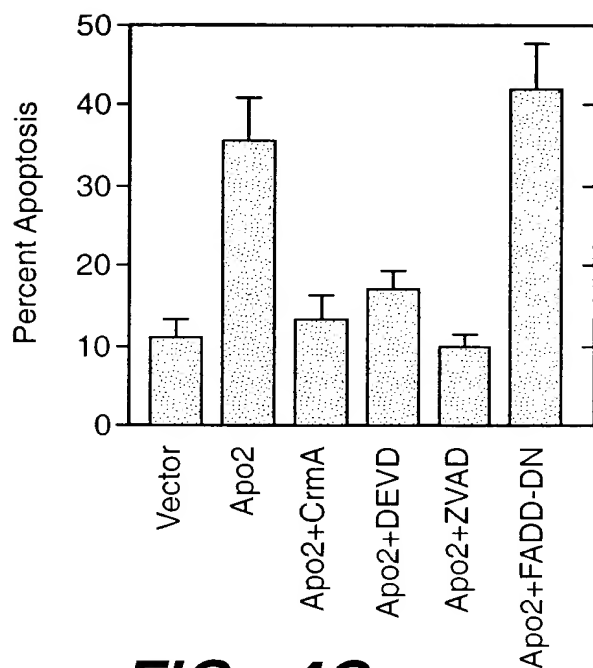


FIG. 4C

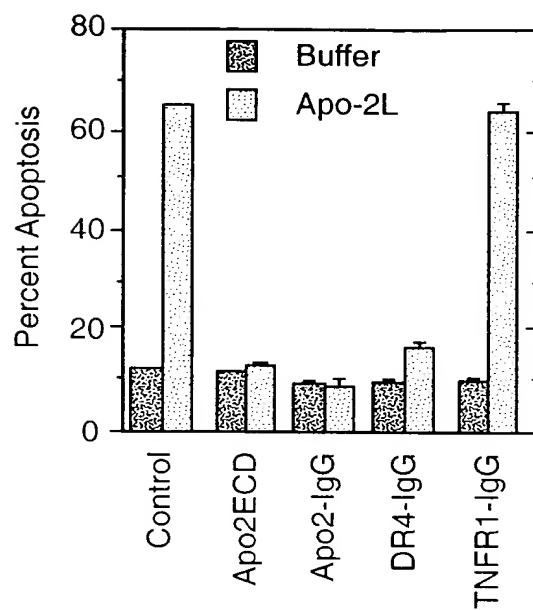


FIG. 4D

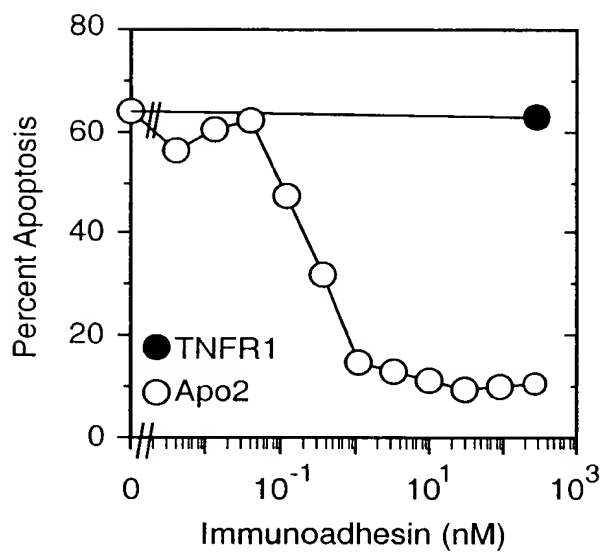


FIG. 4E

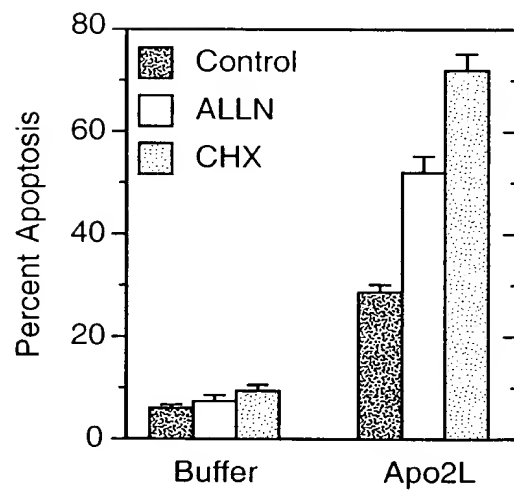


FIG. 5C

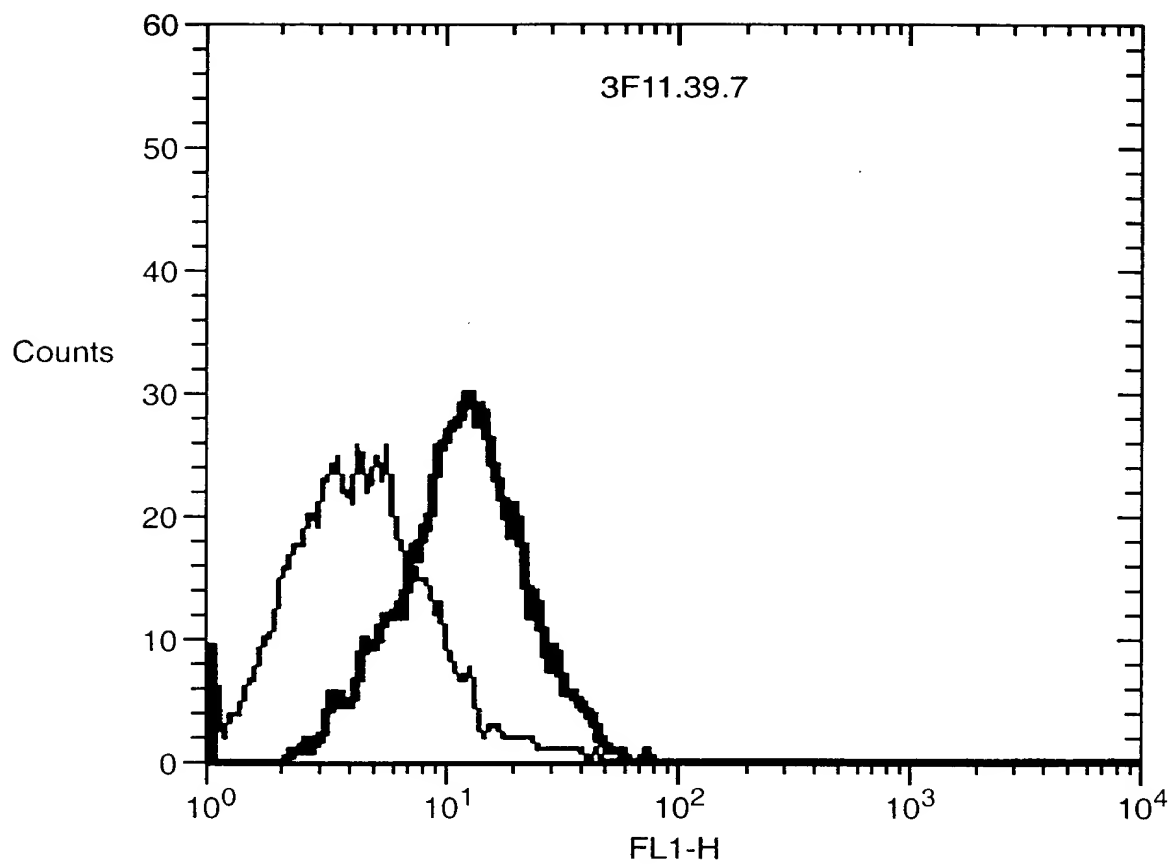


FIG._7

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FIG._8

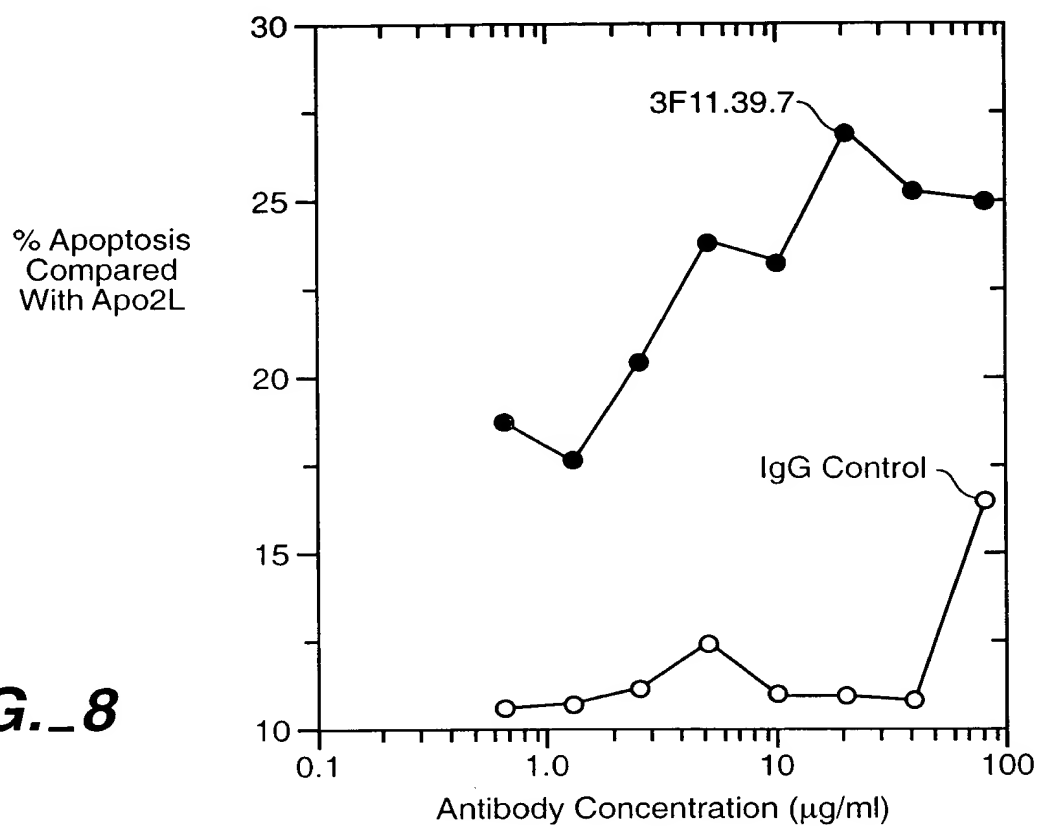


FIG._9

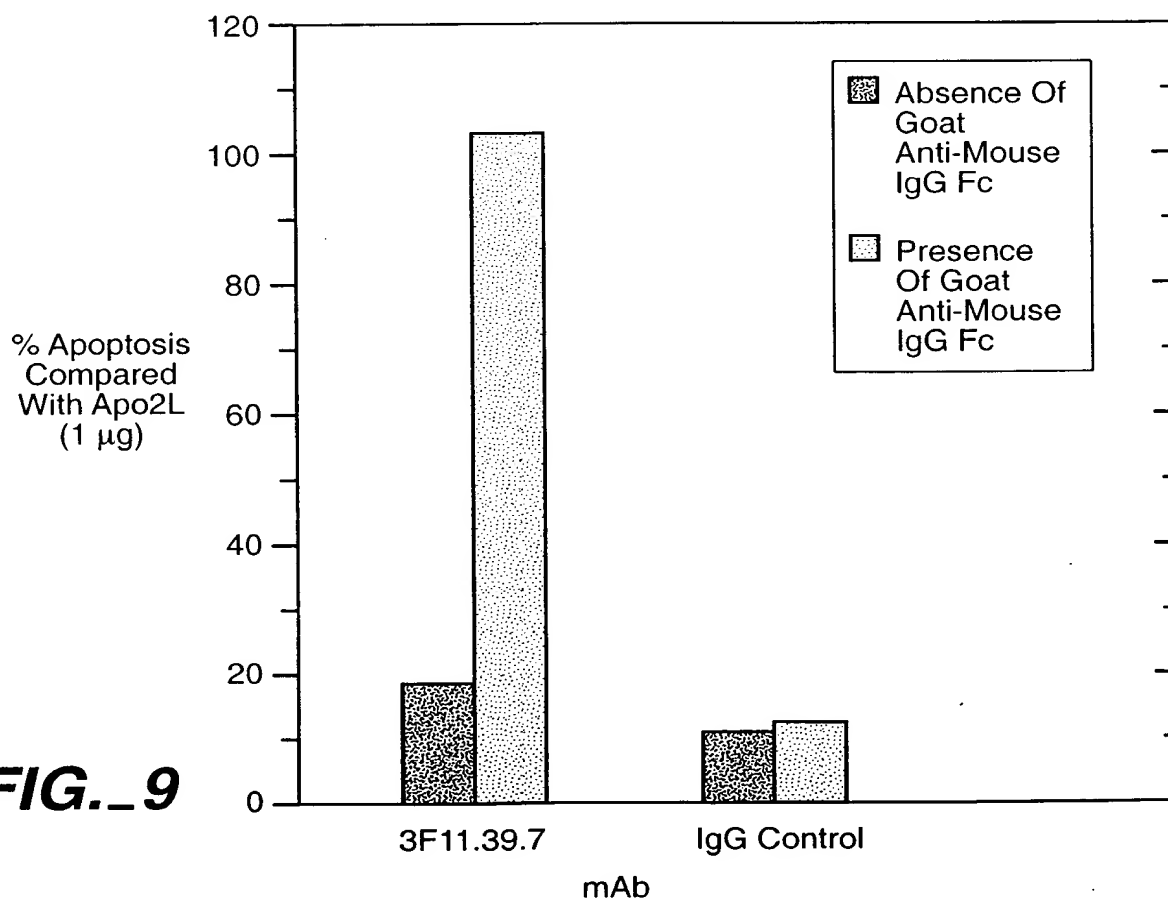


FIG._10

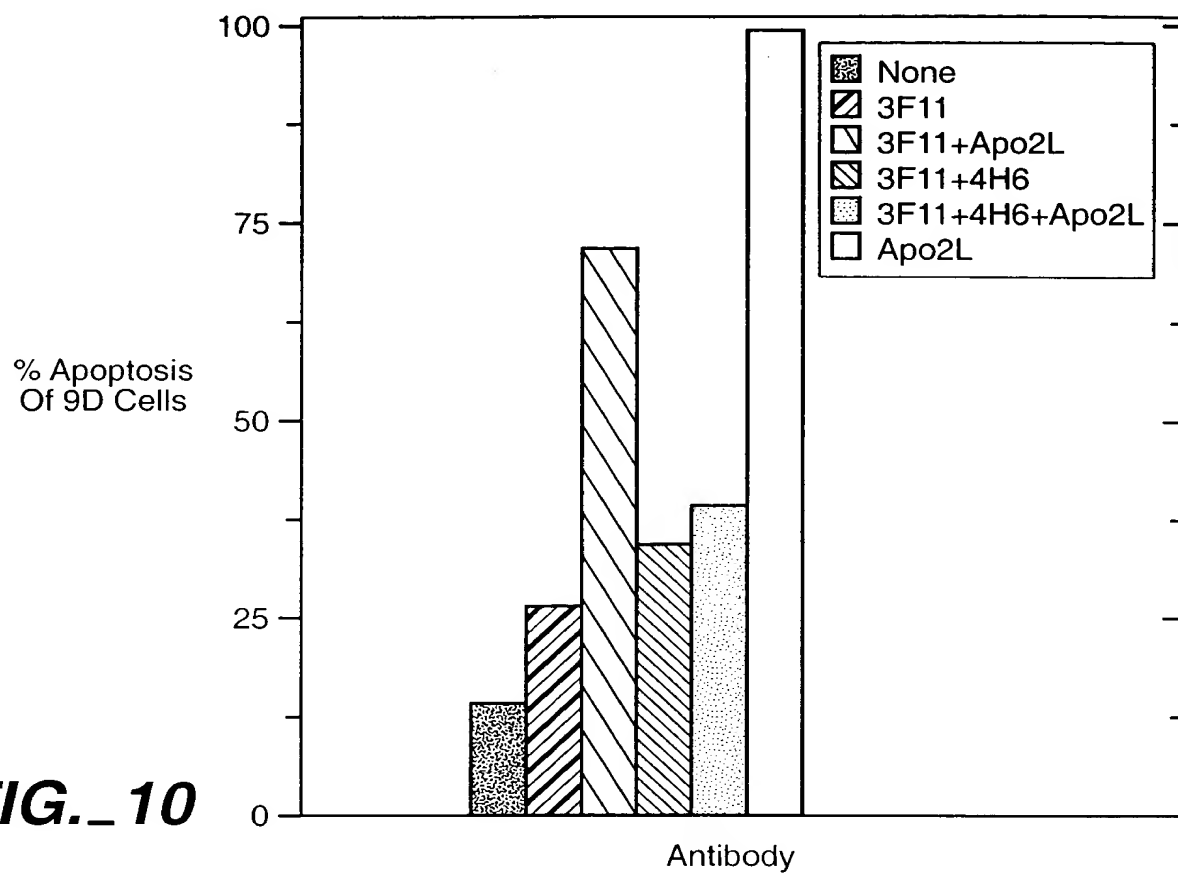
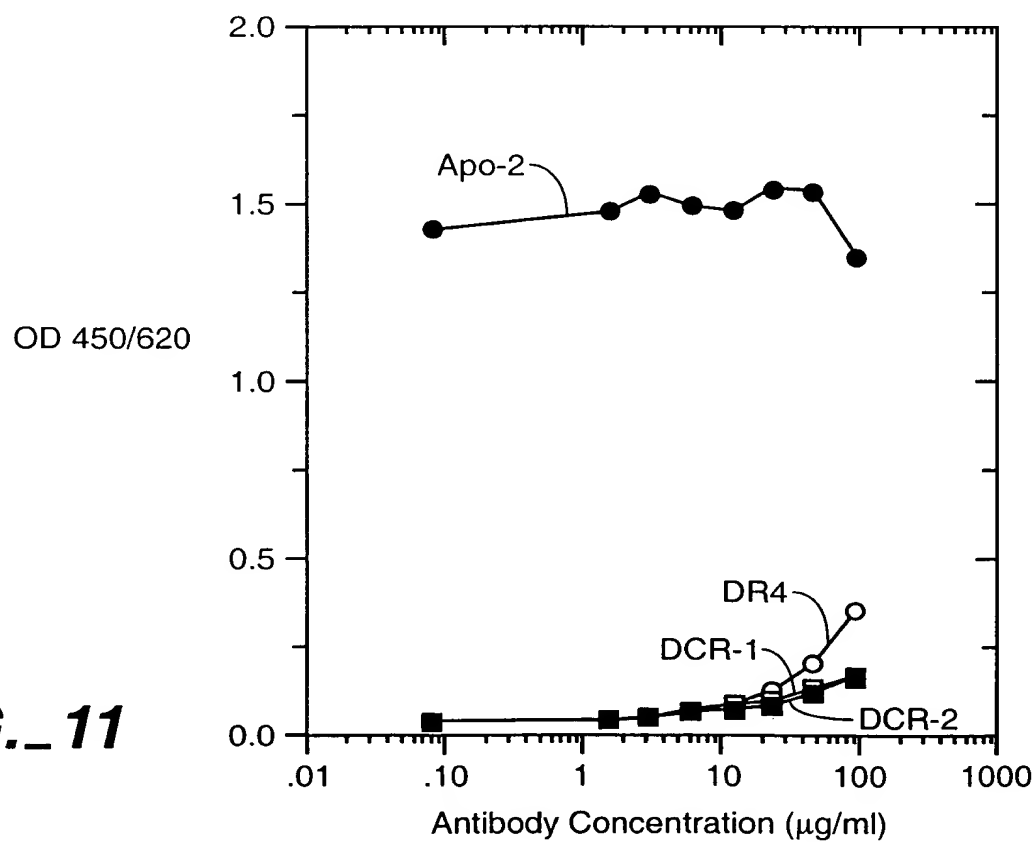


FIG._11





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